

SEQUENCE LISTING

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<120> PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS

<130> 11899.0217.DVUS02

<150> US 09/755,630

<151> 2001-01-05

<150> US 60/174,669

<151> 2000-01-06

<160> 295

<170> PatentIn version 3.2

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Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala
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Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
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Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys
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Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
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Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu
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Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr
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Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu
195 200 205
Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro
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Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser
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 35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
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Ser Leu Glu Lys Arg Glu Ala Glu Ala Gln Leu Gly Glu Met Val Thr

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 35 40 45

Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr
 50 55 60

Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala
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Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln Ile Phe Asn
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Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met
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Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu
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Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val
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Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu Tyr Glu Phe
 180 185 190

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Met Leu Val Ile Gln Lys Met Thr Asp Ala
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Gln Lys Met Thr Asp Tyr Tyr Leu Ser Thr
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Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr
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Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr
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Asp Tyr Tyr Leu Ser Thr Ala Phe Gln Ala
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Ser Thr Ala Phe Gln Ala Leu Asp Ser Lys
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Thr Thr Glu Met Asp Asp Ala Ser Glu Ala
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Asp Asp Ala Ser Glu Ala Asn Met Glu Leu
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Glu Ala Asn Met Glu Leu Leu Val Gln Val
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Glu Leu Leu Val Gln Val Gly Glu Asn Leu
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H: 544092(BNT_01!.DOC)

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Lys	Pro	Val	Ser	Glu	Asp	Asn	Pro	Glu	Thr
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Glu	Asp	Asn	Pro	Glu	Thr	Tyr	Glu	Glu	Ala
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 Arg Phe Ala Lys Leu Leu Ser Asp Arg Lys
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Asp Tyr Phe Asp Val Ile Ala Gly Thr Ser
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H: 544092(BNT_01!.DOC)

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Tyr Leu Arg Val Gln Glu Asn Ala Leu Ala
1 5 10

<210> 204
<211> 10

<212> PRT
<213> Artificial

<220>
<223> Synthetic polypeptide

<400> 204

Tyr Leu Arg Ile Gln Asp Asp Thr Leu Thr
1 5 10

<210> 205
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Synthetic polypeptide

<400> 205

Tyr Leu Thr Val Ala Ala Ala Ala Leu Thr
1 5 10

<210> 206
<211> 10
<212> PRT
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<220>
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<400> 206

Phe Leu Arg Val Gln Glu Asn Ala Leu Thr
1 5 10

<210> 207
<211> 10
<212> PRT
<213> Artificial

<220>
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<400> 207

Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala
1 5 10

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<220>
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<400> 208

Lys Lys Tyr Leu Arg Ile Gln Asp Asp Thr
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 <400> 209

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 1 5 10

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 1 5 10

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 <400> 211

 Ala Thr Tyr Glu Glu Ala Lys Leu Arg Phe
 1 5 10

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 <220>
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 <400> 212

 Glu Ala Tyr Glu Glu Ala Leu Lys Arg Phe
 1 5 10

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<400> 213

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1 5 10

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<211> 10

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<220>

<223> Synthetic polypeptide

<400> 214

Glu Thr Tyr Ala Glu Ala Leu Lys Arg Phe
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<400> 215

Glu Thr Tyr Glu Ala Ala Leu Lys Arg Phe
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<400> 216

Glu Thr Tyr Glu Glu Ala Ala Lys Arg Phe
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<211> 10

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<400> 218

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<210> 219

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<400> 219

Glu Thr Tyr Glu Glu Ala Leu Lys Arg Ala
1 5 10

<210> 220

<211> 10

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<400> 220

Gly Thr Asn Ala Gln Ser Leu Ala Asp Phe
1 5 10

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<400> 221

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<400> 222

Glu Thr Phe Glu Glu Ala Leu Lys Arg Phe
1 5 10

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<400> 223

Tyr	Glu	Glu	Ala	Leu	Lys	Thr	Phe	Ala	Lys
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<211> 10
<212> PRT
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<400> 224

Phe	Glu	Glu	Ala	Leu	Lys	Arg	Phe	Ala	Lys
1				5					10

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<212> PRT
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<220>
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<400> 225

Ala	Ala	Leu	Lys	Arg	Phe	Ala	Lys	Leu	Leu
1				5					10

<210> 226
<211> 10
<212> PRT
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<220>
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<400> 226

Glu	Ala	Ala	Lys	Arg	Phe	Ala	Lys	Leu	Leu
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<212> PRT
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<400> 227

Glu Ala Leu Ala Arg Phe Ala Lys Leu Leu
1 5 10

<210> 228

<211> 10

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<400> 228

Glu Ala Leu Lys Ala Phe Ala Lys Leu Leu
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<210> 229

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<400> 229

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<400> 230

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 <400> 234

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 <400> 235

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 <400> 236

 Asp Phe Ala Lys Gln Leu Ser Asp Glu Arg
 1 5 10

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 <220>
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 <400> 237

 Ala Phe Ala Ala Leu Leu Ser Asp Arg Lys
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 <210> 238
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 <400> 238

 Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro
 1 5 10

 <210> 239
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 <400> 239

 Leu Lys Arg Phe Ala Lys Leu Leu Ser Asp
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 <220>
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 <400> 240

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 <400> 241

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<211> 55

<212> DNA

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<220>

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<400> 242

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<211> 42

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<400> 243

tcccaactgt cctggtccat aagaagcttt gtttgctcgg ag 42

<210> 244

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<211> 39

<212> DNA

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<223> Synthetic construct

<400> 245

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<210> 246

<211> 1128

<212> DNA

<213> Artificial

<220>

<223> Synthetic construct

<400> 246

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gcactggcac tacttcagag tttgataaaa catatacagc aaaagaggca gctacctgga 120

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ctgctgtaca ttggatgtta gttatacaga aaatgactga tgcagcaagt tcttacatga      180
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ttcaagaaaa tgcattaaca ggcacaacta ctgaaatgga tgatgcttct gaggctaata      300
tggaattatt agtacaagtt ggtgaaaact tattgaagaa accagtttcc gaagacaatc      360
ctgaaaccta tgaggaagct ctaaagaggt ttgcaaaatt gctctctgat aggaagaaac      420
tccgagcaaa caaagcttct tatggaccag gacagttggg agaaatgggtg actgttctta      480
gtattgatgg aggtggaatt agaggggatca ttccggctac cattctcgaa tttcttgaag      540
gacaacttca ggaaatggac aataatgcag atgcaagact tgcagattac tttgatgtaa      600
ttggaggaac aagtacagga ggtttattga ctgctatgat aagtactcca aatgaaaaca      660
atcgaccctt tgctgctgcc aaagaaattg taccttttta cttcgaacat ggccctcaga      720
tttttaatcc tagtggtcaa attttaggcc caaaatatga tggaaaatat cttatgcaag      780
ttcttcaaga aaaacttggg gaaactcgtg tgcacaaagc tttgacagaa gttgtcatct      840
caagctttga catcaaaaca aataagccag taatattcac taagtcaaat ttagcaaact      900
ctccagaatt ggatgctaag atgtatgaca taagttattc cacagcagca gtcceaacat      960
attttctctc gcattacttt gttactaata ctagtaatgg agatgaatat gaggttcaatc    1020
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<211> 366

<212> PRT

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<400> 247

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20          25          30
Thr Ala Val His Trp Met Leu Val Ile Gln Lys Met Thr Asp Ala Ala
35          40          45
Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Ala Phe Gln Ala Leu
50          55          60
Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Thr Gly
65          70          75          80
Thr Thr Thr Glu Met Asp Asp Ala Ser Glu Ala Asn Met Glu Leu Leu
85          90          95

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Val Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Glu Asp Asn
 100 105 110
 Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu Ser
 115 120 125
 Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr Gly Pro Gly Gln
 130 135 140
 Leu Gly Glu Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly Ile Arg
 145 150 155 160
 Gly Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu Glu Gly Gln Leu Gln
 165 170 175
 Glu Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe Asp Val
 180 185 190
 Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile Ser Thr
 195 200 205
 Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Glu Ile Val Pro
 210 215 220
 Phe Tyr Phe Glu His Gly Pro Gln Ile Phe Asn Pro Ser Gly Gln Ile
 225 230 235 240
 Leu Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln Glu
 245 250 255
 Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val Ile
 260 265 270
 Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr Lys Ser
 275 280 285
 Asn Leu Ala Asn Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp Ile Ser
 290 295 300
 Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro Pro His Tyr Phe Val
 305 310 315 320
 Thr Asn Thr Ser Asn Gly Asp Glu Tyr Glu Phe Asn Leu Val Asp Gly
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<220>
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<400> 248
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<210> 249

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<212> DNA

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<400> 249

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<210> 250

<211> 1128

<212> DNA

<213> Artificial

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<223> Synthetic construct

<400> 250

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gacttgcaca aaaggatcca gcatttgctt caattaggtc attgaattac aaaaaaatgc 180

tgttgctctc attaggcact ggcaactactt cagagtttga taaaacatat acagcaaaag 240

aggcagctac ctggactgct gtacattgga tgtagttat acagaaaatg actgatgcag 300

caagttctta catgactgat tattaccttt ctactgcttt tcaagctctt gattcaaaaa 360

acaattacct caggggtcaa gaaaatgcat taacaggcac aactactgaa atggatgatg 420

cttctgaggc taatatggaa ttattagtag aagttgggtga aaacttattg aagaaaccag 480

tttccgaaga caatcctgaa acctatgagg aagctctaaa gaggtttgca aaattgctct 540

ctgataggaa gaaactccga gcaaacaaag cttcttatgg accaggacag ttgggagaaa 600

tggtgactgt tcttagtatt gatggaggtg gaattagagg gatcattccg gctaccattc 660

tcgaatttct tgaaggacaa cttcaggaaa tggacaataa tgcagatgca agacttgcag 720

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ctccaaatga aaacaatcga ccctttgctg ctgccaaaga aattgtacct ttttacttcg 840

aacatggccc tcagattttt aatcctagtgt gtcaaatttt aggcccaaaa tatgatggaa 900

aatatcttat gcaagttctt caagaaaaac ttggagaaac tcgtgtgcat caagctttga 960

cagaagttgt catctcaagc tttgacatca aaacaaataa gccagtaata ttcactaagt 1020

caaatttagc aaactctcca gaattggatg ctaagatgta tgacataagt tattccacag 1080

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<210> 251

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<220>
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<400> 251

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20          25          30
Arg Leu Ala Gln Lys Asp Pro Ala Phe Ala Ser Ile Arg Ser Leu Asn
35          40          45
Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly Thr Gly Thr Thr Ser Glu
50          55          60
Phe Asp Lys Thr Tyr Thr Ala Lys Glu Ala Ala Thr Trp Thr Ala Val
65          70          75          80
His Trp Met Leu Val Ile Gln Lys Met Thr Asp Ala Ala Ser Ser Tyr
85          90          95
Met Thr Asp Tyr Tyr Leu Ser Thr Ala Phe Gln Ala Leu Asp Ser Lys
100         105         110
Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Thr Gly Thr Thr Thr
115         120         125
Glu Met Asp Asp Ala Ser Glu Ala Asn Met Glu Leu Leu Val Gln Val
130         135         140
Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Glu Asp Asn Pro Glu Thr
145         150         155         160
Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu Ser Asp Arg Lys
165         170         175
Lys Leu Arg Ala Asn Lys Ala Ser Tyr Gly Pro Gly Gln Leu Gly Glu
180         185         190
Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile
195         200         205
Pro Ala Thr Ile Leu Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp
210         215         220
Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly
225         230         235         240
Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu
245         250         255
Asn Asn Arg Pro Phe Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe
260         265         270
Glu His Gly Pro Gln Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro
61
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Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly				
290		295		300
Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe				
305		310		315
320				
Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala				
		325		330
				335
Asn Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr				
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				350
Ala Ala Ala Pro Thr Tyr Phe Pro Pro His Tyr Phe Val Thr				
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				365

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<220>
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<220>
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<400> 253
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 gtgctgttgc tactgttgct gatccggcgt tattatccat tagcgttgca acgagacttg 180
 cacaaaagga tccagcattt gttcaatta ggtcattgaa ttacaaaaaa atgctgttgc 240
 tctcattagg cactggcact acttcagagt ttgataaaac atatacagca aaagaggcag 300
 ctacctggac tgctgtacat tggatgtag ttatacagaa aatgactgat gcagcaagtt 360
 cttacatgac tgattattac ctttctactg cttttcaagc tcttgattca aaaaacaatt 420

acctcagggt tcaagaaaat gcattaacag gcacaactac tgaaatggat gatgcttctg 480
aggctaatat ggaattatta gtacaagttg gtgaaaactt attgaagaaa ccagtttccg 540
aagacaatcc tgaacacctat gaggaagctc taaagagggt tgcaaaattg ctctctgata 600
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ctgttcttag tattgatgga ggtggaatta gagggatcat tccggctacc attctcgaat 720
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gccctcagat ttttaatcct agtgggtcaaa ttttaggcc aaaatatgat ggaaaatc 960
ttatgcaagt tcttcaagaa aaacttgag aaactcgtgt gcatcaagct ttgacagaag 1020
ttgtcatctc aagctttgac atcaaaacaa ataagccagt aatattcact aagtcaaatt 1080
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<210> 255

<211> 366

<212> PRT

<213> Artificial

<220>

<223> Synthetic polypeptide

<400> 255

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			20					25					30		
Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro	Ala	Leu	Leu	Ser	Ile	Ser	Val
		35					40					45			
Ala	Thr	Arg	Leu	Ala	Gln	Lys	Asp	Pro	Ala	Phe	Ala	Ser	Ile	Arg	Ser
		50				55					60				
Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr
65					70					75				80	
Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala	Lys	Glu	Ala	Ala	Thr	Trp	Thr
			85						90					95	
Ala	Val	His	Trp	Met	Leu	Val	Ile	Gln	Lys	Met	Thr	Asp	Ala	Ala	Ser
			100					105					110		
Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Leu	Ser	Thr	Ala	Phe	Gln	Ala	Leu	Asp
		115					120					125			
Ser	Lys	Asn	Asn	Tyr	Leu	Arg	Val	Gln	Glu	Asn	Ala	Leu	Thr	Gly	Thr
	130					135					140				

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 Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Glu Asp Asn Pro
 165 170 175
 Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu Ser Asp
 180 185 190
 Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr Gly Pro Gly Gln Leu
 195 200 205
 Gly Glu Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly Ile Arg Gly
 210 215 220
 Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu Glu Gly Gln Leu Gln Glu
 225 230 235 240
 Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe Asp Val Ile
 245 250 255
 Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile Ser Thr Pro
 260 265 270
 Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Glu Ile Val Pro Phe
 275 280 285
 Tyr Phe Glu His Gly Pro Gln Ile Phe Asn Pro Ser Gly Gln Ile Leu
 290 295 300
 Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln Glu Lys
 305 310 315 320
 Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val Ile Ser
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 340 345 350
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 355 360 365

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 <211> 55
 <212> DNA
 <213> Artificial

<220>
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 aaaatgcatt aacaggcaca actactgaaa tggatgatgc ttctgaggct aatatggaat 240
 tattagtaca agttggtgaa aacttattga agaaaccagt ttccgaagac aatcctgaaa 300
 cctatgagga agctctaaag aggtttgcaa aattgctctc tgataggaag aaactccgat 360
 caaacaagc ttcttatgga ccaggacagt tgggagaaat ggtgactggt cttagtattg 420
 atggaggtgg aattagaggg atcattccgg ctaccattct cgaatttctt gaaggacaac 480
 ttcaggaaat ggacaataat gcagatgcaa gacttgcala ttactttgat gtaattggag 540
 gaacaagtac aggaggttta ttgactgcta tgataagtac tccaaatgaa aacaatcgac 600
 cctttgctgc tgccaaagaa attgtacctt ttacttcga acatggccct cagattttta 660
 atcctagtgg tcaaatttta ggcccaaat atgatggaaa atatcttatg caagttcttc 720
 aagaaaaact tggagaaact cgtgtgcatc aagctttgac agaagttgtc atctcaagct 780
 ttgacatcaa aacaaataag ccagtaatat tcactaagtc aaatttagca aactctccag 840
 aattggatgc taagatgtat gacataagtt attccacagc agcagctcca acatattttc 900
 ctccgcatta ctttgttact aatactagta atggagatga atatgagttc aatcttggtg 960
 atggtgctgt tgctactggt gctgatccgg cgttattatc cattagcgtt gcaacgagac 1020
 ttgcacaaaa ggatccagca tttgcttcaa ttaggtcatt gaattacaaa aaaatgctgt 1080
 tgctctcatt aggcactggc actacttcag agtttgataa ataatgag 1128

<210> 259
 <211> 366
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic polypeptide

<400> 259

Thr	Tyr	Thr	Ala	Lys	Glu	Ala	Ala	Thr	Trp	Thr	Ala	Val	His	Trp	Met	1	5	10	15
Leu	Val	Ile	Gln	Lys	Met	Thr	Asp	Ala	Ala	Ser	Ser	Tyr	Met	Thr	Asp	20	25	30	
Tyr	Tyr	Leu	Ser	Thr	Ala	Phe	Gln	Ala	Leu	Asp	Ser	Lys	Asn	Asn	Tyr	35	40	45	
Leu	Arg	Val	Gln	Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp	50	55	60	
Asp	Ala	Ser	Glu	Ala	Asn	Met	Glu	Leu	Leu	Val	Gln	Val	Gly	Glu	Asn	65	70	75	
Leu	Leu	Lys	Lys	Pro	Val	Ser	Glu	Asp	Asn	Pro	Glu	Thr	Tyr	Glu	Glu	85	90	95	
Ala	Leu	Lys	Arg	Phe	Ala	Lys	Leu	Leu	Ser	Asp	Arg	Lys	Lys	Leu	Arg	100	105	110	
Ser	Asn	Lys	Ala	Ser	Tyr	Gly	Pro	Gly	Gln	Leu	Gly	Glu	Met	Val	Thr	115	120	125	
Val	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Ile	Arg	Gly	Ile	Ile	Pro	Ala	Thr	130	135	140	
Ile	Leu	Glu	Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Met	Asp	Asn	Asn	Ala	145	150	155	
Asp	Ala	Arg	Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr	165	170	175	
Gly	Gly	Leu	Leu	Thr	Ala	Met	Ile	Ser	Thr	Pro	Asn	Glu	Asn	Asn	Arg	180	185	190	
Pro	Phe	Ala	Ala	Ala	Lys	Glu	Ile	Val	Pro	Phe	Tyr	Phe	Glu	His	Gly	195	200	205	
Pro	Gln	Ile	Phe	Asn	Pro	Ser	Gly	Gln	Ile	Leu	Gly	Pro	Lys	Tyr	Asp	210	215	220	
Gly	Lys	Tyr	Leu	Met	Gln	Val	Leu	Gln	Glu	Lys	Leu	Gly	Glu	Thr	Arg	225	230	235	
Val	His	Gln	Ala	Leu	Thr	Glu	Val	Val	Ile	Ser	Ser	Phe	Asp	Ile	Lys	245	250	255	
Thr	Asn	Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Asn	Ser	Pro	260	265	270	
Glu	Leu	Asp	Ala	Lys	Met	Tyr	Asp	Ile	Ser	Tyr	Ser	Thr	Ala	Ala	Ala	275	280	285	
Pro	Thr	Tyr	Phe	Pro	Pro	His	Tyr	Phe	Val	Thr	Asn	Thr	Ser	Asn	Gly	290	295	300	
Asp	Glu	Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Ala	305	310	315	
Asp	Pro	Ala	Leu	Leu	Ser	Ile	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Lys				

	325		330		335										
Asp	Pro	Ala	Phe	Ala	Ser	Ile	Arg	Ser	Leu	Asn	Tyr	Lys	Lys	Met	Leu
			340					345					350		
Leu	Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr	Ser	Glu	Phe	Asp	Lys		
			355				360					365			

<210> 260
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic construct

 <400> 260
 ggagctcgag aaaagagagg ctgaagctaa tgcattaaca ggcacaacta ctgaa 55

 <210> 261
 <211> 39
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic construct

 <400> 261
 ggtctagagg aattctcatt attcttgaac cctgaggta 39

 <210> 262
 <211> 1128
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic construct

 <400> 262
 tcgagaaaag agaggctgaa gctaattgcat taacaggcac aactactgaa atggatgatg 60
 cttctgaggc taatatggaa ttattagtagc aagttgggtga aaacttattg aagaaaccag 120
 tttccgaaga caatcctgaa acctatgagg aagctctaaa gaggtttgca aaattgctct 180
 ctgataggaa gaaactccga gcaaacaag cttcttatgg accaggacag ttgggagaaa 240
 tgggtgactgt tcttagtatt gatggagggtg gaattagagg gatcattccg gctaccattc 300
 tcgaatttct tgaaggacaa cttcaggaaa tggacaataa tgcagatgca agacttgcag 360
 attactttga tgtaattgga ggaacaagta caggagggtt attgactgct atgataagta 420
 ctccaaatga aaacaatcga ccctttgctg ctgccaaaga aattgtacct ttttacttcg 480
 aacatggccc tcagattttt aatcctagtgt gtcaaatttt aggcccaaaa tatgatggaa 540
 aatatcttat gcaagttctt caagaaaaac ttggagaaac tcgtgtgcat caagctttga 600
 cagaagttgt catctcaagc tttgacatca aaacaaataa gccagtaata ttcactaagt 660

caaathtagc aaactctcca gaattggatg ctaagatgta tgacataagt tattccacag 720
 cagcagctcc aacatatattt cctccgcatt actttgttac taatactagt aatggagatg 780
 aatatgagtt caatcttggt gatggtgctg ttgctactgt tgctgatccg gcgttattat 840
 ccattagcgt tgcaacgaga cttgcacaaa aggatccagc atttgcttca attaggtcat 900
 tgaattacaa aaaaatgctg ttgctctcat taggcactgg cactacttca gagtttgata 960
 aaacatatac agcaaaagag gcagctacct ggactgctgt acattggatg ttagttatac 1020
 agaaaatgac tgatgcagca agttcttaca tgactgatta ttacctttct actgcttttc 1080
 aagctcttga ttcaaaaaac aattacctca gggttcaaga ataatgag 1128

<210> 263

<211> 366

<212> PRT

<213> Artificial

<220>

<223> Synthetic polypeptide

<400> 263

Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu Ala
 1 5 10 15

Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys Pro
 20 25 30

Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe
 35 40 45

Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser
 50 55 60

Tyr Gly Pro Gly Gln Leu Gly Glu Met Val Thr Val Leu Ser Ile Asp
 65 70 75 80

Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu
 85 90 95

Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala Arg Leu Ala
 100 105 110

Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr
 115 120 125

Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala
 130 135 140

Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln Ile Phe Asn
 145 150 155 160

Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met
 165 170 175

Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu
 180 185 190

Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val
 195 200 205
 Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu Asp Ala Lys
 210 215 220
 Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro
 225 230 235 240
 Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu Tyr Glu Phe
 245 250 255
 Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro Ala Leu Leu
 260 265 270
 Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro Ala Phe Ala
 275 280 285
 Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly
 290 295 300
 Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala Lys Glu Ala
 305 310 315 320
 Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln Lys Met Thr
 325 330 335
 Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Ala Phe
 340 345 350
 Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln Glu
 355 360 365

<210> 264
 <211> 1158
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 264
 atggccacca ccaagagctt cctcactctg atcttcatga tcctggccac caccagcagc 60
 accttcgccc agctcggcga gatggtgacc gtgctctcca tcgacggcgg tggcatcagg 120
 ggcatcatcc cggccaccat cctggagttc ctggagggcc aactccagga gatggacaac 180
 aacgccgacg cccgcctggc cgactacttc gacgtgatcg gtggcaccag caccggcggt 240
 ctctgaccg ccatgatctc cactccgaac gagaacaacc gccccttcgc cgctgcgaag 300
 gagatcgtcc cgttctactt cgaacacggc cctcagattt tcaaccctc ggggtcaaac 360
 ctgggccccca agtacgacgg caagtacctt atgcaagtgc ttcaggagaa gctgggagag 420
 actaggggtgc accaggcgct gaccgaggtc gtcacttcca gcttcgacat caagaccaac 480
 aagccagtca tcttcaccaa gtccaacctg gccaacagcc cggagctgga cgctaagatg 540

tacgacatct cctactccac tgctgccgct cccacgtact tccctccgca ctacttcgtc 600
 accaacacca gcaacggcga cgagtacgag ttcaaccttg ttgacgggtgc ggtggctacg 660
 gtggcgggacc cggcgtcct gtccatcagc gtcgccacgc gcttggccca gaaggatcca 720
 gccttcgcta gcattaggag cctcaactac aagaagatgc tgctgctcag cctgggcact 780
 ggcacgacct ccgagttcga caagacctac actgccaaagg aggccgctac ctggaccgcc 840
 gtccattgga tgctgggtcat ccagaagatg acggacgccg cttccagcta catgaccgac 900
 tactacctct ccaactgcgtt ccaggcgctt gactccaaga acaactacct ccgtgttcag 960
 gagaatgcc tcaactggcac cagcaccgag atggacgatg cctccgaggc caacatggag 1020
 ctgctcgtcc aggtgggtga gaacctcctg aagaagcccg tctccgaaga caatcccag 1080
 acctatgagg aagcgctcaa gcgctttgcc aagctgctct ctgataggaa gaaactccgc 1140
 gctaacaagg ccagctac 1158

<210> 265

<211> 386

<212> PRT

<213> Artificial

<220>

<223> Synthetic polypeptide

<400> 265

Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala
 1 5 10 15

Thr Thr Ser Ser Thr Phe Ala Gln Leu Gly Glu Met Val Thr Val Leu
 20 25 30

Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu
 35 40 45

Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala
 50 55 60

Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
 65 70 75 80

Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe
 85 90 95

Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln
 100 105 110

Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys
 115 120 125

Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
 130 135 140

Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn
 145 150 155 160

Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu
 165 170 175
 Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr
 180 185 190
 Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu
 195 200 205
 Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro
 210 215 220
 Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro
 225 230 235 240
 Ala Phe Ala Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu
 245 250 255
 Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala
 260 265 270
 Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln
 275 280 285
 Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser
 290 295 300
 Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln
 305 310 315 320
 Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
 325 330 335
 Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys
 340 345 350
 Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg
 355 360 365
 Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala
 370 375 380

Ser Tyr
 385

<210> 266
 <211> 55
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 266
 ggagctcgag aaaagagagg ctgaagctag cctcaactac aagaagatgc tgctg

55

<210> 267
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 267
 gccgagctgt cctggtccgt agctggcctt gttagcgcg ag 42

<210> 268
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 268
 gccagctacg gaccaggaca gctcggcgag atggtg 36

<210> 269
 <211> 39
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 269
 ggtctagagg aattctcatt acctaattgct agcgaaggc 39

<210> 270
 <211> 1167
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 270
 atggccacca ccaagagctt cctcatcctg atcttcatga tcttggccac caccagcagc 60
 accttcgcca gcctcaacta caagaagatg ctgctgctca gcctgggcac tggcacgacc 120
 tccgagttcg acaagaccta cactgccaaag gaggccgcta cctggaccgc cgtccattgg 180
 atgctggtca tccagaagat gacggacgcc gcttcagct acatgaccga ctactacctc 240
 tccactgctg tccaggcgct tgactccaag aacaactacc tccgtgttca ggagaatgcc 300
 ctactggca ccacgaccga gatggacgat gcctccgagg ccaacatgga gctgctcgtc 360
 caggtgggtg agaacctcct gaagaagccc gtctccgaag acaatcccga gacctatgag 420
 gaagcgctca agcgctttgc caagctgctc tctgatagga agaaactccg cgctaacaag 480
 gccagctacg gaccaggaca gctcggcgag atggtgaccg tgctctccat cgacggcggt 540
 ggcatcaggg gcatcatccc ggccaccatc ctggagttcc tggagggcca actccaggag 600
 atggacaaca acgccgacgc ccgcctggcc gactacttcg acgtgatcgg tggcaccagc 660
 accggcggtc tcttgaccgc catgatctcc actccgaacg agaacaaccg ccccttcgcc 720

gctgcgaagg agatcgcccc gttctacttc gaacacggcc ctcagatttt caaccctcgc 780
 ggtcaaatcc tgggccccaa gtacgacggc aagtacctta tgcaagtgc ttaggagaag 840
 ctgggcgaga ctaggggtgca ccaggcgctg accgaggtcg tcattctccag cttcgacatc 900
 aagaccaaca agccagtcac cttcaccaag tccaacctgg ccaacagccc ggagctggac 960
 gctaagatgt acgacatctc ctactccact gctgccgctc ccacgtactt ccctccgcac 1020
 tacttcgtca ccaacaccag caacggcgac gactacgagt tcaaccttgt tgacgggtgcg 1080
 gtggctacgg tggcggaccc ggcgctcctg tccatcagcg tcgccacgcg cctggcccag 1140
 aaggatccag ccttcgctag cattagg 1167

<210> 271
 <211> 389
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic polypeptide

<400> 271

Met	Ala	Thr	Thr	Lys	Ser	Phe	Leu	Ile	Leu	Ile	Phe	Met	Ile	Leu	Ala
1				5					10					15	
Thr	Thr	Ser	Ser	Thr	Phe	Ala	Ser	Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu
			20					25					30		
Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr	Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr
		35					40					45			
Ala	Lys	Glu	Ala	Ala	Thr	Trp	Thr	Ala	Val	His	Trp	Met	Leu	Val	Ile
	50					55					60				
Gln	Lys	Met	Thr	Asp	Ala	Ser	Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Leu	
65				70					75					80	
Ser	Thr	Ala	Phe	Gln	Ala	Leu	Asp	Ser	Lys	Asn	Asn	Tyr	Leu	Arg	Val
				85					90					95	
Gln	Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser
			100					105					110		
Glu	Ala	Asn	Met	Glu	Leu	Leu	Val	Gln	Val	Gly	Glu	Asn	Leu	Leu	Lys
	115						120					125			
Lys	Pro	Val	Ser	Glu	Asp	Asn	Pro	Glu	Thr	Tyr	Glu	Glu	Ala	Leu	Lys
	130					135					140				
Arg	Phe	Ala	Lys	Leu	Leu	Ser	Asp	Arg	Lys	Lys	Leu	Arg	Ala	Asn	Lys
145				150						155				160	
Ala	Ser	Tyr	Gly	Pro	Gly	Gln	Leu	Gly	Glu	Met	Val	Thr	Val	Leu	Ser
				165				170						175	
Ile	Asp	Gly	Gly	Gly	Ile	Arg	Gly	Ile	Ile	Pro	Ala	Thr	Ile	Leu	Glu

180					185					190					
Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Met	Asp	Asn	Asn	Ala	Asp	Ala	Arg
	195						200					205			
Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Leu
	210					215					220				
Leu	Thr	Ala	Met	Ile	Ser	Thr	Pro	Asn	Glu	Asn	Asn	Arg	Pro	Phe	Ala
	225					230					235				240
Ala	Ala	Lys	Glu	Ile	Val	Pro	Phe	Tyr	Phe	Glu	His	Gly	Pro	Gln	Ile
				245					250					255	
Phe	Asn	Pro	Ser	Gly	Gln	Ile	Leu	Gly	Pro	Lys	Tyr	Asp	Gly	Lys	Tyr
			260					265					270		
Leu	Met	Gln	Val	Leu	Gln	Glu	Lys	Leu	Gly	Glu	Thr	Arg	Val	His	Gln
		275					280					285			
Ala	Leu	Thr	Glu	Val	Val	Ile	Ser	Ser	Phe	Asp	Ile	Lys	Thr	Asn	Lys
	290					295					300				
Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Asn	Ser	Pro	Glu	Leu	Asp
	305					310					315				320
Ala	Lys	Met	Tyr	Asp	Ile	Ser	Tyr	Ser	Thr	Ala	Ala	Ala	Pro	Thr	Tyr
				325					330					335	
Phe	Pro	Pro	His	Tyr	Phe	Val	Thr	Asn	Thr	Ser	Asn	Gly	Asp	Glu	Tyr
			340					345					350		
Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro	Ala
		355					360					365			
Leu	Leu	Ser	Ile	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Lys	Asp	Pro	Ala
	370					375					380				
Phe	Ala	Ser	Ile	Arg											
	385														

<210> 272
 <211> 55
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 272
 ggagctcgag aaaagagagg ctgaagctac tgccaaggag gccgctacct ggacc

55

<210> 273
 <211> 39
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic construct

<400> 273
 H: 544092(BNT_011.DOC)

ggtctagagg aattctcatt acttgtcgaa ctccgagggt

39

<210> 274

<211> 1167

<212> DNA

<213> Artificial

<220>

<223> Synthetic construct

<400> 274

atggccacca ccaagagctt cctcatcctg atcttcatga tcctggccac caccagcagc	60
accttcgccca cctacactgc caaggaggcc gctacctgga ccgccgtcca ttggatgctg	120
gtcatccaga agatgacgga cgccgcttcc agctacatga ccgactacta cctctccact	180
gcgttccagg cgcttgactc caagaacaac tacctccgtg ttcaggagaa tgccctcact	240
ggcaccacga ccgagatgga cgatgcctcc gaggccaaca tggagctgct cgtccagggtg	300
ggtgagaacc tcctgaagaa gcccgctctcc gaagacaatc ccgagaccta tgaggaagcg	360
ctcaagcgct ttgccaaagt gctctctgat aggaagaaac tccgcgctaa caaggccagc	420
tacggaccag gacagctcgg cgagatgggt accgtgctct ccacgcacgg cggtggcatc	480
agggggcatca tcccggccac catcctggag ttcttgaggg gccaaactcca ggagatggac	540
aacaacgccg acgcccgcct ggccgactac ttcgacgtga tcggtggcac cagcaccggc	600
ggtctcctga ccgccatgat ctccactccg aacgagaaca accgcccctt cgccgctgcg	660
aaggagatcg tcccgttcta cttcgaacac ggccctcaga ttttcaaccc ctccgggtcaa	720
atcctggggc ccaagtacga cggcaagtac cttatgcaag tgcttcagga gaagctgggc	780
gagactaggg tgcaccaggc gctgaccgag gtcgtcatct ccagcttcga catcaagacc	840
aacaagccag tcattcttcac caagtccaac ctggccaaca gcccgagct ggacgctaag	900
atgtacgaca tctctactc cactgctgcc gctcccacgt acttcctcc gcactacttc	960
gtcaccaaca ccagcaacgg cgacgagtac gagttcaacc ttgttgacgg tgcggtggct	1020
acggtggcgg acccggcgct cctgtccatc agcgtcgcca cgcgctggc ccagaaggat	1080
ccagccttcg ctagcattag gagcctcaac tacaagaaga tgctgctgct cagcctgggc	1140
actggcacga cctccgagtt cgacaag	1167

<210> 275

<211> 389

<212> PRT

<213> Artificial

<220>

<223> Synthetic polypeptide

<400> 275

Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala
 1 5 10 15
 Thr Thr Ser Ser Thr Phe Ala Thr Tyr Thr Ala Lys Glu Ala Ala Thr
 20 25 30
 Trp Thr Ala Val His Trp Met Leu Val Ile Gln Lys Met Thr Asp Ala
 35 40 45
 Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Ala Phe Gln Ala
 50 55 60
 Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Thr
 65 70 75 80
 Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu Ala Asn Met Glu Leu
 85 90 95
 Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Glu Asp
 100 105 110
 Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu
 115 120 125
 Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr Gly Pro Gly
 130 135 140
 Gln Leu Gly Glu Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly Ile
 145 150 155 160
 Arg Gly Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu Glu Gly Gln Leu
 165 170 175
 Gln Glu Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe Asp
 180 185 190
 Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile Ser
 195 200 205
 Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Glu Ile Val
 210 215 220
 Pro Phe Tyr Phe Glu His Gly Pro Gln Ile Phe Asn Pro Ser Gly Gln
 225 230 235 240
 Ile Leu Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln
 245 250 255
 Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val
 260 265 270
 Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr Lys
 275 280 285
 Ser Asn Leu Ala Asn Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp Ile
 290 295 300
 Ser Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro Pro His Tyr Phe
 305 310 315 320
 Val Thr Asn Thr Ser Asn Gly Asp Glu Tyr Glu Phe Asn Leu Val Asp

	325		330		335										
Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro	Ala	Leu	Leu	Ser	Ile	Ser	Val
		340					345						350		
Ala	Thr	Arg	Leu	Ala	Gln	Lys	Asp	Pro	Ala	Phe	Ala	Ser	Ile	Arg	Ser
		355					360					365			
Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr
	370					375					380				
Ser	Glu	Phe	Asp	Lys											
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1															
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1				5					10					15	
Thr	Thr	Ser	Ser	Thr	Cys	Ala	Lys	Leu	Glu	Glu	Met	Val	Thr	Val	Leu
			20					25					30		
Ser	Ile	Asp	Gly	Gly	Gly	Ile	Lys	Gly	Ile	Ile	Pro	Ala	Ile	Ile	Leu
		35					40					45			
Glu	Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Val	Asp	Asn	Asn	Lys	Asp	Ala
	50					55					60				
Arg	Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr	Gly	Gly
65					70					75					80

Leu Leu Thr Ala Met Ile Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe
 85 90 95
 Ala Ala Ala Lys Asp Ile Val Pro Phe Tyr Phe Glu His Gly Pro His
 100 105 110
 Ile Phe Asn Tyr Ser Gly Ser Ile Ile Gly Pro Met Tyr Asp Gly Lys
 115 120 125
 Tyr Leu Leu Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
 130 135 140
 Gln Ala Leu Thr Glu Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn
 145 150 155 160
 Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu
 165 170 175
 Asp Ala Lys Met Tyr Asp Ile Cys Tyr Ser Thr Ala Ala Ala Pro Ile
 180 185 190
 Tyr Phe Pro Pro His Tyr Phe Ile Thr His Thr Ser Asn Gly Asp Ile
 195 200 205
 Tyr Glu Phe Asn Leu Val Asp Gly Gly Val Ala Thr Val Gly Asp Pro
 210 215 220
 Ala Leu Leu Ser Leu Ser Val Ala Thr Arg Leu Ala Gln Glu Asp Pro
 225 230 235 240
 Ala Phe Ser Ser Ile Lys Ser Leu Asp Tyr Lys Gln Met Leu Leu Leu
 245 250 255
 Ser Leu Gly Thr Gly Thr Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala
 260 265 270
 Gln Glu Ala Ala Lys Trp Gly Pro Leu Arg Trp Met Leu Ala Ile Gln
 275 280 285
 Gln Met Thr Asn Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Ile Ser
 290 295 300
 Thr Val Phe Gln Ala Arg His Ser Gln Asn Asn Tyr Leu Arg Val Gln
 305 310 315 320
 Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
 325 330 335
 Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Thr Leu Leu Lys Lys
 340 345 350
 Pro Val Ser Lys Asp Ser Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg
 355 360 365
 Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala
 370 375 380
 Ser Tyr
 385

<210> 279
 <211> 386
 <212> PRT
 <213> Solanum tuberosum

<400> 279

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Met Ala Thr Thr Lys Ser Val Leu Val Leu Phe Phe Met Ile Leu Ala
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Thr Thr Ser Ser Thr Cys Ala Thr Leu Gly Glu Met Val Thr Val Leu
          20          25          30

Ser Ile Asp Gly Gly Gly Ile Lys Gly Ile Ile Pro Ala Thr Ile Leu
          35          40          45

Glu Phe Leu Glu Gly Gln Leu Gln Glu Val Asp Asn Asn Lys Asp Ala
          50          55          60

Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
65          70          75          80

Leu Leu Thr Ala Met Ile Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe
          85          90          95

Ala Ala Ala Lys Asp Ile Val Pro Phe Tyr Phe Glu His Gly Pro His
          100          105          110

Ile Phe Asn Ser Ser Gly Ser Ile Phe Gly Pro Met Tyr Asp Gly Lys
          115          120          125

Tyr Phe Leu Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
          130          135          140

Gln Ala Leu Thr Glu Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn
145          150          155          160

Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu
          165          170          175

Asp Ala Lys Met Asn Asp Ile Cys Tyr Ser Thr Ala Ala Ala Pro Thr
          180          185          190

Tyr Phe Pro Pro His Tyr Phe Val Thr His Thr Ser Asn Gly Asp Lys
          195          200          205

Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Gly Asp Pro
          210          215          220

Ala Leu Leu Ser Leu Ser Val Arg Thr Lys Leu Ala Gln Val Asp Pro
225          230          235          240

Lys Phe Ala Ser Ile Lys Ser Leu Asn Tyr Asn Glu Met Leu Leu Leu
          245          250          255

Ser Leu Gly Thr Gly Thr Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala
          260          265          270

Glu Glu Ala Ala Lys Trp Gly Pro Leu Arg Trp Ile Leu Ala Ile Gln
          275          280          285

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Gln Met Thr Asn Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser
 290 295 300
 Thr Val Phe Gln Ala Arg His Ser Gln Asn Asn Tyr Leu Arg Val Gln
 305 310 315 320
 Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
 325 330 335
 Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Lys Leu Leu Lys Lys
 340 345 350
 Pro Val Ser Lys Asp Ser Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg
 355 360 365
 Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala
 370 375 380
 Ser Tyr
 385
 <210> 280
 <211> 365
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 <213> Solanum tuberosum
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 20 25 30
 Leu Gln Lys Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe
 35 40 45
 Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile
 50 55 60
 Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Asn Glu Ile
 65 70 75 80
 Val Pro Phe Tyr Phe Glu His Gly Pro His Ile Phe Asn Ser Arg Tyr
 85 90 95
 Trp Pro Ile Phe Trp Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val
 100 105 110
 Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu
 115 120 125
 Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe
 130 135 140
 Thr Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu Asp Ala Lys Thr Tyr
 145 150 155 160
 Asp Ile Cys Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro Pro His
 165 170 175

Tyr Phe Ala Thr Asn Thr Ile Asn Gly Asp Lys Tyr Glu Phe Asn Leu
 180 185 190
 Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro Ala Leu Leu Ser Val
 195 200 205
 Ser Val Ala Thr Arg Arg Ala Gln Glu Asp Pro Ala Phe Ala Ser Ile
 210 215 220
 Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly Thr Gly
 225 230 235 240
 Thr Thr Ser Glu Phe Asp Lys Thr His Thr Ala Glu Glu Thr Ala Lys
 245 250 255
 Trp Gly Ala Leu Gln Trp Met Leu Val Ile Gln Gln Met Thr Glu Ala
 260 265 270
 Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Val Phe Gln Asp
 275 280 285
 Leu His Ser Gln Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Thr
 290 295 300
 Gly Thr Thr Thr Lys Ala Asp Asp Ala Ser Glu Ala Asn Met Glu Leu
 305 310 315 320
 Leu Ala Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Lys Asp
 325 330 335
 Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu
 340 345 350
 Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr
 355 360 365
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 <211> 364
 <212> PRT
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 <400> 281
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 Ile Lys Gly Ile Ile Pro Ala Ile Ile Leu Glu Phe Leu Glu Gly Gln
 20 25 30
 Leu Gln Glu Val Asp Asn Asn Lys Asp Ala Arg Leu Ala Asp Tyr Phe
 35 40 45
 Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile
 50 55 60
 Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Asp Ile
 65 70 75 80
 Val Pro Phe Tyr Phe Glu His Gly Pro His Ile Phe Asn Tyr Ser Gly
 85 90 95

Ser Ile Leu Gly Pro Met Tyr Asp Gly Lys Tyr Leu Leu Gln Val Leu
 100 105 110
 Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val
 115 120 125
 Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr
 130 135 140
 Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp
 145 150 155 160
 Ile Cys Tyr Ser Thr Ala Ala Ala Pro Ile Tyr Phe Pro Pro His His
 165 170 175
 Phe Val Thr His Thr Ser Asn Gly Ala Arg Tyr Glu Phe Asn Leu Val
 180 185 190
 Asp Gly Ala Val Ala Thr Val Gly Asp Pro Ala Leu Leu Ser Leu Ser
 195 200 205
 Val Ala Thr Arg Leu Ala Gln Glu Asp Pro Ala Phe Ser Ser Ile Lys
 210 215 220
 Ser Leu Asp Tyr Lys Gln Met Leu Leu Leu Ser Leu Gly Thr Gly Thr
 225 230 235 240
 Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala Glu Glu Ala Ala Lys Trp
 245 250 255
 Gly Pro Leu Arg Trp Met Leu Ala Ile Gln Gln Met Thr Asn Ala Ala
 260 265 270
 Ser Phe Tyr Met Thr Asp Tyr Tyr Ile Ser Thr Val Phe Gln Ala Arg
 275 280 285
 His Ser Gln Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Asn Gly
 290 295 300
 Thr Thr Thr Glu Met Asp Asp Ala Ser Glu Ala Asn Met Glu Leu Leu
 305 310 315 320
 Val Gln Val Gly Glu Thr Leu Leu Lys Lys Pro Val Ser Arg Asp Ser
 325 330 335
 Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu Ser
 340 345 350
 Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr
 355 360
 <210> 282
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 <212> PRT
 <213> Solanum tuberosum
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Thr Thr Ser Ser Thr Cys Ala Lys Leu Glu Glu Met Val Thr Val Leu
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 Ser Ile Asp Gly Gly Gly Ile Lys Gly Ile Ile Pro Ala Ile Ile Leu
 35 40 45
 Glu Phe Leu Glu Gly Gln Leu Gln Glu Val Asp Asn Asn Lys Asp Ala
 50 55 60
 Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
 65 70 75 80
 Leu Leu Thr Ala Met Ile Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe
 85 90 95
 Ala Ala Ala Lys Asp Ile Val Pro Phe Tyr Phe Glu His Gly Pro His
 100 105 110
 Ile Phe Asn Tyr Ser Gly Ser Ile Leu Gly Pro Met Tyr Asp Gly Lys
 115 120 125
 Tyr Leu Leu Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
 130 135 140
 Gln Ala Leu Thr Glu Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn
 145 150 155 160
 Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu
 165 170 175
 Asp Ala Lys Met Tyr Asp Ile Cys Tyr Ser Thr Ala Ala Ala Pro Ile
 180 185 190
 Tyr Phe Pro Pro His His Phe Val Thr His Thr Ser Asn Gly Ala Arg
 195 200 205
 Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Gly Asp Pro
 210 215 220
 Ala Leu Leu Ser Leu Ser Val Ala Thr Arg Leu Ala Gln Glu Asp Pro
 225 230 235 240
 Ala Phe Ser Ser Ile Lys Ser Leu Asp Tyr Lys Gln Met Leu Leu Leu
 245 250 255
 Ser Leu Gly Thr Gly Thr Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala
 260 265 270
 Glu Glu Ala Ala Lys Trp Gly Pro Leu Arg Trp Met Leu Ala Ile Gln
 275 280 285
 Gln Met Thr Asn Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Ile Ser
 290 295 300
 Thr Val Phe Gln Ala Arg His Ser Gln Asn Asn Tyr Leu Arg Val Gln
 305 310 315 320
 Glu Asn Ala Leu Asn Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
 325 330 335
 Ala Asn Met Glu Leu Leu Val Gln Val Gly Ala Thr Leu Leu Lys Lys

340	345	350
Pro Val Ser Lys Asp Ser Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg		
355	360	365
Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala		
370	375	380

Ser Tyr
385

<210> 283
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Synthetic polypeptide

<400> 283

Ala Phe Phe Asp Lys Thr Tyr Thr Ala Lys
1 5 10

<210> 284
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Synthetic polypeptide

<400> 284

Cys Ile Phe Asp Ser Thr Tyr Thr Ala Lys
1 5 10

<210> 285
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<212> DNA
<213> Solanum tuberosum

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acatttgctc agttgggaga aatggtgact gttcttagta ttgatggagg tggaattaga	120
gggatcattc cggctaccat tctcgaattt cttgaaggac aacttcagga aatggacaat	180
aatgcagatg caagacttgc agattacttt gatgtaattg gaggaacaag tacaggaggt	240
ttattgactg ctatgataag tactccaaat gaaaacaatc gaccctttgc tgctgccaaa	300
gaaattgtac ctttttactt cgaacatggc cctcagattt ttaatcctag tgggtcaaatt	360
ttaggcccaa aatatgatgg aaaatatctt atgcaagttc ttcaagaaaa acttgagaga	420
actcgtgtgc atcaagcttt gacagaagtt gtcattctcaa gctttgacat caaaacaaat	480
aagccagtaa tattcactaa gtcaaattta gcaaactctc cagaattgga tgctaagatg	540

tatgacataa gttattccac agcagcagct ccaacatatt ttcttccgca ttactttgtt 600
 actaatacta gtaatggaga tgaatatgag ttcaatcttg ttgatgggtgc tgttgctact 660
 gttgctgatac cggcggttatt atccattagc gttgcaacga gacttgcaca aaaggatcca 720
 gcatttgctt caattagggtc attgaattac aaaaaaatgc tgttgctctc attaggcact 780
 ggactacttt cagagtttga taaaacatat acagcaaaaag aggcagctac ctggactgct 840
 gtacattgga tgtagttat acagaaaatg actgatgcag caagttctta catgactgat 900
 tattaccttt ctactgcttt tcaagctctt gattcaaaaa acaattacct caggggttcaa 960
 gaaaatgcat taacaggcac aactactgaa atggatgatg cttctgaggc taatatggaa 1020
 ttattagtac aagttggtga aaacttattg aagaaaccag tttccgaaga caatcctgaa 1080
 acctatgagg aagctctaaa gaggtttgca aaattgctct ctgataggaa gaaactccga 1140
 gcaaacaaaag cttcttatta a 1161

<210> 286

<211> 386

<212> PRT

<213> Solanum tuberosum

<400> 286

Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala
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 Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu
 35 40 45
 Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala
 50 55 60
 Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
 65 70 75 80
 Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe
 85 90 95
 Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln
 100 105 110
 Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys
 115 120 125
 Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
 130 135 140
 Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn
 145 150 155 160
 Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu
 165 170 175

Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr
 180 185 190
 Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu
 195 200 205
 Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro
 210 215 220
 Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro
 225 230 235 240
 Ala Phe Ala Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu
 245 250 255
 Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala
 260 265 270
 Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln
 275 280 285
 Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser
 290 295 300
 Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln
 305 310 315 320
 Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
 325 330 335
 Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys
 340 345 350
 Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg
 355 360 365
 Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala
 370 375 380
 Ser Tyr
 385

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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic polypeptide

<400> 287

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 20 25 30
 Gly Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg Gly
 35 40 45

Ile Ile Pro Gly Val Ile Leu Lys Gln Leu Glu Ala Thr Leu Gln Arg
 50 55 60
 Trp Asp Ser Ser Ala Arg Leu Ala Glu Tyr Phe Asp Val Val Ala Gly
 65 70 75 80
 Thr Ser Thr Gly Gly Ile Ile Thr Ala Ile Leu Thr Ala Pro Asp Pro
 85 90 95
 Gln Asn Lys Asp Arg Pro Leu Tyr Ala Ala Glu Glu Ile Ile Asp Phe
 100 105 110
 Tyr Ile Glu His Gly Pro Ser Ile Phe Asn Lys Ser Thr Ala Cys Ser
 115 120 125
 Leu Pro Gly Ile Phe Cys Pro Lys Tyr Asp Gly Lys Tyr Leu Gln Glu
 130 135 140
 Ile Ile Ser Gln Lys Leu Asn Glu Thr Leu Leu Asp Gln Thr Thr Thr
 145 150 155 160
 Asn Val Val Ile Pro Ser Phe Asp Ile Lys Leu Leu Arg Pro Thr Ile
 165 170 175
 Phe Ser Thr Phe Lys Leu Glu Glu Val Pro Glu Leu Asn Val Lys Leu
 180 185 190
 Ser Asp Val Cys Met Gly Thr Ser Ala Ala Pro Ile Val Phe Pro Pro
 195 200 205
 Tyr Tyr Phe Lys His Gly Asp Thr Glu Phe Asn Leu Val Asp Gly Ala
 210 215 220
 Ile Ile Ala Asp Ile Pro Ala Pro Val Ala Leu Ser Glu Val Leu Gln
 225 230 235 240
 Gln Glu Lys Tyr Lys Asn Lys Glu Ile Leu Leu Leu Ser Ile Gly Thr
 245 250 255
 Gly Val Val Lys Pro Gly Glu Gly Tyr Ser Ala Asn Arg Thr Trp Thr
 260 265 270
 Ile Phe Asp Trp Ser Ser Glu Thr Leu Ile Gly Leu Met Gly His Gly
 275 280 285
 Thr Arg Ala Met Ser Asp Tyr Tyr Val Gly Ser His Phe Lys Ala Leu
 290 295 300
 Gln Pro Gln Asn Asn Tyr Leu Arg Ile Gln Glu Tyr Asp Leu Asp Pro
 305 310 315 320
 Ala Leu Glu Ser Ile Asp Asp Ala Ser Thr Glu Asn Met Glu Asn Leu
 325 330 335
 Glu Lys Val Gly Gln Ser Leu Leu Asn Glu Pro Val Lys Arg Met Asn
 340 345 350
 Leu Asn Thr Phe Val Val Glu Glu Thr Gly Glu Gly Thr Asn Ala Glu
 355 360 365

Ala Leu Asp Arg Leu Ala Gln Ile Leu Tyr Glu Glu Lys Ile Thr Arg
370 375 380

Gly Leu Gly Lys Ile Ser Leu Glu Val Asp Asn Ile Asp Pro Tyr Thr
385 390 395 400

Glu Arg Val Arg Lys Leu Leu Phe
405

<210> 288
<211> 410
<212> PRT
<213> Zea mays

<400> 288

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Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly
20 25 30

Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu
35 40 45

Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr
50 55 60

Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu Ala Ser Met
65 70 75 80

Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe Ala Ala Lys Asp
85 90 95

Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile Phe Pro Gln Lys
100 105 110

Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu Gly Leu Val Arg
115 120 125

Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys Ile Lys Ser Leu
130 135 140

Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn Val Ile Val Pro
145 150 155 160

Ala Phe Asp Val Lys Tyr Leu Gln Pro Ile Ile Phe Ser Thr Tyr Glu
165 170 175

Ala Lys Thr Asp Thr Leu Lys Asn Ala His Leu Ser Asp Ile Cys Ile
180 185 190

Ser Thr Ser Ala Ala Pro Thr Tyr Phe Pro Ala His Phe Phe Lys Thr
195 200 205

Glu Ala Thr Asp Gly Arg Pro Pro Arg Glu Tyr His Leu Val Asp Gly
210 215 220

Gly Val Ala Ala Asn Asn Pro Thr Met Val Ala Met Ser Met Leu Thr
225 230 235 240

Leu Ala Ser Met Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe
 115 120 125
 Ala Ala Lys Asp Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile
 130 135 140
 Phe Pro Gln Lys Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu
 145 150 155 160
 Gly Leu Val Arg Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys
 165 170 175
 Ile Lys Ser Leu Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn
 180 185 190
 Val Ile Val Pro Ala Phe Asp Val Lys Tyr Leu Gln Pro Ile Ile Phe
 195 200 205
 Ser Thr Tyr Glu Ala Lys Thr Asp Ala Leu Lys Asn Ala His Leu Ser
 210 215 220
 Asp Ile Cys Ile Ser Thr Ser Ala Ala Pro Thr Tyr Phe Pro Ala His
 225 230 235 240
 Phe Phe Lys Thr Glu Ala Thr Asp Gly Arg Pro Pro Arg Glu Tyr His
 245 250 255
 Leu Val Asp Gly Gly Val Ala Ala Asn Asn Pro Thr Met Val Ala Met
 260 265 270
 Ser Met Leu Thr Lys Glu Val His Arg Arg Asn Pro Asn Phe Asn Ala
 275 280 285
 Gly Ser Pro Thr Glu Tyr Thr Asn Tyr Leu Ile Ile Ser Val Gly Thr
 290 295 300
 Gly Ser Ala Lys Gln Ala Glu Lys Tyr Thr Ala Glu Gln Cys Ala Lys
 305 310 315 320
 Trp Gly Leu Ile Gln Trp Leu Tyr Asn Gly Gly Phe Thr Pro Ile Ile
 325 330 335
 Asp Ile Phe Ser His Ala Ser Ser Asp Met Val Asp Ile His Ala Ser
 340 345 350
 Ile Leu Phe Gln Ala Leu His Cys Glu Lys Lys Tyr Leu Arg Ile Gln
 355 360 365
 Leu Tyr Tyr Ala Gly Tyr Phe Asp Trp Glu Arg Ile Val Arg Gly His
 370 375 380
 Arg His Gln Gly Glu His Gly Val Ser Asp Ile Asp Arg Pro Gly Ala
 385 390 395 400
 Ala Gln Glu Ala Ser Gly Glu Ser Glu His Arg His Arg Ala Val Arg
 405 410 415
 Val Leu Arg Arg Gly His Lys Cys Thr Val Ala Ser Leu Arg Gln Ala
 420 425 430
 Thr Leu Arg Ala Gln Ala Thr Gln Glu Gln Ser Gln Leu Gln Leu Ile

435		440		445
Asn Thr Ser Leu Ser His Ser Met Cys Ser Phe Arg Arg Phe Thr Val				
450		455		460
Ser Tyr Phe Phe Asn Phe Asn Ser Val Cys Val Leu Cys Val Leu Cys				
465		470		475
Val Tyr Gln Thr Phe Lys Phe Asn Gln Lys Lys Lys Lys Lys Lys Lys				
	485		490	495
Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Ala Ala				
	500		505	
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<213> Zea mays				
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Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly				
	20		25	30
Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu				
	35		40	45
Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr				
	50		55	60
Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu Ala Ser Met				
65	70		75	80
Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe Ala Ala Lys Asp				
	85		90	95
Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile Phe Pro Gln Lys				
	100		105	110
Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu Gly Leu Val Arg				
	115		120	125
Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys Ile Lys Ser Leu				
	130		135	140
Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn Val Ile Val Pro				
145	150		155	160
Ala Phe Asp Val Lys Ser Leu Gln Pro Ile Ile Phe Ser Thr Tyr Glu				
	165		170	175
Ala Lys Thr Asp Thr Leu Lys Asn Ala His Leu Ser Asp Ile Cys Ile				
	180		185	190
Ser Thr Ser Ala Ala Pro Thr Tyr Phe Pro Ala His Phe Phe Lys Thr				
	195		200	205

210	215	220
Gly Val Ala Ala Asn Asn Pro Thr Met Val Ala Met Ser Met Leu Thr 225 230 235 240		
Lys Glu Val His Arg Arg Asn Pro Asn Phe Asn Ala Gly Ser Pro Thr 245 250 255		
Glu Tyr Thr Asn Tyr Leu Ile Ile Ser Val Gly Thr Gly Ser Ala Lys 260 265 270		
Gln Ala Glu Lys Tyr Thr Ala Glu Gln Cys Ala Lys Trp Gly Leu Ile 275 280 285		
Gln Trp Leu Tyr Asn Gly Gly Phe Thr Pro Ile Ile Asp Ile Phe Ser 290 295 300		
His Ala Ser Ser Asp Met Val Asp Ile His Ala Ser Ile Leu Phe Gln 305 310 315 320		
Ala Leu His Cys Glu Lys Lys Tyr Leu Arg Ile Gln Asp Asp Thr Leu 325 330 335		
Thr Gly Asn Ala Ser Ser Val Asp Ile Ala Thr Lys Glu Asn Met Glu 340 345 350		
Ser Leu Ile Ser Ile Gly Gln Glu Leu Leu Asn Lys Pro Val Ala Arg 355 360 365		
Val Asn Ile Asp Thr Gly Leu Tyr Glu Ser Cys Glu Gly Glu Gly Thr 370 375 380		
Asn Ala Gln Ser Leu Ala Asp Phe Ala Lys Gln Leu Ser Asp Glu Arg 385 390 395 400		
Lys Leu Arg Lys Ser Asn Leu Asn Ser Asn 405 410		

<210> 291
 <211> 410
 <212> PRT
 <213> Zea mays

<400> 291

Met Gly Ser Ile Gly Arg Gly Thr Ala Asn Cys Ala Thr Val Pro Gln 1 5 10 15
Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly 20 25 30
Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu 35 40 45
Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr 50 55 60
Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu Ala Ser Met 65 70 75 80
Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe Ala Ala Lys Asp

Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile Phe Pro Gln Lys
 100 105 110
 Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu Gly Leu Val Arg
 115 120 125
 Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys Ile Lys Ser Leu
 130 135 140
 Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn Val Ile Val Pro
 145 150 155 160
 Ala Phe Asp Val Lys Tyr Leu Gln Pro Ile Ile Phe Ser Thr Tyr Glu
 165 170 175
 Ala Lys Thr Asp Ala Leu Lys Asn Ala His Leu Ser Asp Ile Cys Ile
 180 185 190
 Ser Thr Ser Ala Ala Pro Thr Tyr Phe Pro Ala His Phe Phe Lys Thr
 195 200 205
 Glu Ala Thr Asp Gly Arg Pro Pro Arg Glu Tyr His Leu Val Asp Gly
 210 215 220
 Gly Val Ala Ala Asn Asn Pro Thr Met Val Ala Met Ser Met Leu Thr
 225 230 235 240
 Lys Glu Val His Arg Arg Asn Pro Asn Phe Asn Ala Gly Ser Pro Thr
 245 250 255
 Glu Tyr Thr Asn Tyr Leu Ile Ile Ser Val Gly Thr Gly Ser Ala Lys
 260 265 270
 Gln Ala Glu Lys Tyr Thr Ala Glu Gln Cys Ala Lys Trp Gly Leu Ile
 275 280 285
 Gln Trp Leu Tyr Asn Gly Gly Phe Thr Pro Ile Ile Asp Ile Phe Ser
 290 295 300
 His Ala Ser Ser Asp Met Val Asp Ile His Ala Ser Ile Leu Phe Gln
 305 310 315 320
 Ala Leu His Cys Glu Lys Lys Tyr Leu Arg Ile Gln Asp Asp Thr Leu
 325 330 335
 Thr Gly Asn Ala Ser Ser Val Asp Ile Ala Thr Lys Glu Asn Met Glu
 340 345 350
 Ser Leu Ile Ser Ile Gly Gln Glu Leu Leu Lys Lys Pro Val Ala Arg
 355 360 365
 Val Asn Ile Asp Thr Gly Leu Tyr Glu Ser Cys Asp Gly Glu Gly Thr
 370 375 380
 Asn Ala Gln Ser Leu Ala Asp Phe Ala Lys Gln Leu Ser Asp Glu Arg
 385 390 395 400
 Lys Leu Arg Lys Ser Asn Leu Asn Ser Asn
 405 410

<210> 292
 <211> 410
 <212> PRT
 <213> Zea mays

<400> 292

Met	Gly	Ser	Ile	Gly	Arg	Gly	Thr	Ala	Asn	Cys	Ala	Thr	Val	Pro	Gln	1	5	10	15
Pro	Pro	Pro	Ser	Thr	Gly	Lys	Leu	Ile	Thr	Ile	Leu	Ser	Ile	Asp	Gly	20	25	30	
Gly	Gly	Ile	Arg	Gly	Leu	Ile	Pro	Ala	Thr	Ile	Ile	Ala	Tyr	Leu	Glu	35	40	45	
Ala	Lys	Leu	Gln	Glu	Leu	Asp	Gly	Pro	Asp	Ala	Arg	Ile	Ala	Asp	Tyr	50	55	60	
Phe	Asp	Val	Ile	Ala	Gly	Thr	Ser	Thr	Gly	Ala	Leu	Leu	Ala	Ser	Met	65	70	75	80
Leu	Ala	Ala	Pro	Asp	Glu	Asn	Asn	Arg	Pro	Leu	Phe	Ala	Ala	Lys	Asp	85	90	95	
Leu	Thr	Thr	Phe	Tyr	Leu	Glu	Asn	Gly	Pro	Lys	Ile	Phe	Pro	Gln	Lys	100	105	110	
Lys	Ala	Gly	Leu	Leu	Thr	Pro	Leu	Arg	Asn	Leu	Leu	Gly	Leu	Val	Arg	115	120	125	
Gly	Pro	Lys	Tyr	Asp	Gly	Val	Phe	Leu	His	Asp	Lys	Ile	Lys	Ser	Leu	130	135	140	
Thr	His	Asp	Val	Arg	Val	Ala	Asp	Thr	Val	Thr	Asn	Val	Ile	Val	Pro	145	150	155	160
Ala	Phe	Asp	Val	Lys	Ser	Leu	Gln	Pro	Ile	Ile	Phe	Ser	Thr	Tyr	Glu	165	170	175	
Ala	Lys	Thr	Asp	Thr	Leu	Lys	Asn	Ala	His	Leu	Ser	Asp	Ile	Cys	Ile	180	185	190	
Ser	Thr	Ser	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Ala	His	Phe	Phe	Lys	Ile	195	200	205	
Glu	Ala	Thr	Asp	Gly	Arg	Pro	Pro	Arg	Glu	Tyr	His	Leu	Val	Asp	Gly	210	215	220	
Gly	Val	Ala	Ala	Asn	Asn	Pro	Thr	Met	Val	Ala	Met	Ser	Met	Leu	Thr	225	230	235	240
Lys	Glu	Val	His	Arg	Arg	Asn	Pro	Asn	Phe	Asn	Ala	Gly	Ser	Pro	Thr	245	250	255	
Glu	Tyr	Thr	Asn	Tyr	Leu	Ile	Ile	Ser	Val	Gly	Thr	Gly	Ser	Ala	Lys	260	265	270	
Gln	Ala	Glu	Lys	Tyr	Thr	Ala	Glu	Gln	Cys	Ala	Lys	Trp	Gly	Leu	Ile	275	280	285	

Gln Trp Leu Tyr Asn Gly Gly Phe Thr Pro Ile Ile Asp Ile Phe Ser
 290 295 300

His Ala Ser Ser Asp Met Val Asp Ile His Ala Ser Ile Leu Phe Gln
 305 310 315 320

Ala Leu His Cys Glu Lys Lys Tyr Leu Arg Ile Gln Asp Asp Thr Leu
 325 330 335

Thr Gly Asn Ala Ser Ser Val Asp Ile Ala Thr Lys Glu Asn Met Glu
 340 345 350

Ser Leu Ile Ser Ile Gly Gln Glu Leu Leu Asn Lys Pro Val Ala Arg
 355 360 365

Val Asn Ile Asp Thr Gly Leu Tyr Glu Ser Cys Glu Gly Glu Gly Thr
 370 375 380

Asn Ala Gln Ser Leu Ala Asp Phe Ala Lys Gln Leu Ser Asp Glu Arg
 385 390 395 400

Lys Leu Arg Lys Ser Asn Leu Asn Ser Asn
 405 410

<210> 293
 <211> 337
 <212> PRT
 <213> Zea mays

<400> 293

Met Gly Ser Ile Gly Arg Gly Thr Ala Asn Cys Ala Thr Val Pro Gln
 1 5 10 15

Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly
 20 25 30

Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu
 35 40 45

Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr
 50 55 60

Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu Ala Ser Met
 65 70 75 80

Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe Ala Ala Lys Asp
 85 90 95

Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile Phe Pro Gln Lys
 100 105 110

Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu Gly Leu Val Arg
 115 120 125

Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys Ile Lys Ser Leu
 130 135 140

Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn Val Ile Val Pro
 145 150 155 160

Ala Phe Asp Val Lys Tyr Leu Gln Pro Ile Ile Phe Ser Thr Tyr Glu
165 170 175

Ala Lys Thr Asp Ala Leu Lys Asn Ala His Leu Ser Asp Ile Cys Ile
180 185 190

Ser Thr Ser Ala Ala Pro Thr Tyr Phe Pro Ala His Phe Phe Lys Thr
195 200 205

Glu Ala Thr Asp Gly Arg Pro Pro Arg Glu Tyr His Leu Val Asp Gly
210 215 220

Gly Val Ala Ala Asn Asn Pro Thr Met Val Ala Met Ser Met Leu Thr
225 230 235 240

Lys Glu Val His Arg Arg Asn Pro Asn Phe Asn Ala Gly Ser Pro Thr
245 250 255

Glu Tyr Thr Asn Tyr Leu Ile Ile Ser Val Gly Thr Gly Ser Ala Lys
260 265 270

Gln Ala Glu Lys Tyr Thr Ala Glu Gln Cys Ala Lys Trp Gly Leu Ile
275 280 285

Gln Trp Leu Tyr Asn Gly Gly Phe Thr Pro Ile Ile Asp Ile Phe Ser
290 295 300

His Ala Ser Ser Asp Met Val Asp Ile His Ala Ser Ile Leu Phe Gln
305 310 315 320

Ala Leu His Cys Glu Lys Lys Tyr Leu Arg Ile Gln Leu Tyr Tyr Ala
325 330 335

Gly

<210> 294
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Synthetic construct

<400> 294
gggccatggc gcagttggga gaaatggtg

29

<210> 295
<211> 37
<212> DNA
<213> Artificial

<220>
<223> Synthetic construct

<400> 295
aacaagctt cttattgagg tgcggccgct tgcatgc

37